

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/780,703

Source: IFWO

Date Processed by STIC: 10/18/04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/780,703

TIME: 10:07:07

Input Set : A:\012670-105.ST25.txt

Output Set: N:\CRF4\09282004\J780703.raw

```

4 <110> APPLICANT: Lee, Jong Seob
5      Kim, Yun Hee
6      Choi, Eun kyung
7      Yoo, So Yeon
8      Ahn, Ji Hoon
9      Choi, Yang Do
11 <120> TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and
Method for
12      Manipulating Flowering Time of Plant Using the Same
14 <130> FILE REFERENCE: 012679-105
16 <140> CURRENT APPLICATION NUMBER: US 10/780,703
17 <141> CURRENT FILING DATE: 2004-02-19
19 <150> PRIOR APPLICATION NUMBER: KR 10-2003-10772
20 <151> PRIOR FILING DATE: 2003-02-20
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <211> LENGTH: 1140
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis thaliana
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)...(1137)
34 <223> OTHER INFORMATION: cDNA of LOV1 gene
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38 Met Ala Ile Val Ser Ser Thr Thr Ser Ile Ile Pro Met Ser Asn Gln
39 1          5          10          15
41 gtc aac aat aac gaa aaa ggt ata gaa gac aat gat cat aga ggc ggc      96
42 Val Asn Asn Asn Glu Lys Gly Ile Glu Asp Asn Asp His Arg Gly Gly
43          20          25          30
45 caa gag agt cat gtc caa aat gaa gat gaa gct gat gat cat gat cat      144
46 Gln Glu Ser His Val Gln Asn Glu Asp Glu Ala Asp Asp His Asp His
47          35          40          45
49 gac atg gtc atg ccc gga ttt aga ttc cat cct acc gaa gaa gaa ctc      192
50 Asp Met Val Met Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu
51          50          55          60
53 ata gag ttt tac ctt cgc cga aaa gtt gaa ggc aaa cgc ttt aat gta      240
54 Ile Glu Phe Tyr Leu Arg Arg Lys Val Glu Gly Lys Arg Phe Asn Val
55          65          70          75          80
57 gaa ctc atc act ttc ctc gat ctt tat cgc tat gat cct tgg gaa ctt      288
58 Glu Leu Ile Thr Phe Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Glu Leu
59          85          90          95
61 cct gct atg gcg gcg ata gga gag aaa gag tgg tac ttc tat gtg cca      336

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62 Pro Ala Met Ala Ala Ile Gly Glu Lys Glu Trp Tyr Phe Tyr Val Pro
63          100          105          110
65 aga gat cgg aaa tat aga aat gga gat aga ccg aac cga gta acg act 384
66 Arg Asp Arg Lys Tyr Arg Asn Gly Asp Arg Pro Asn Arg Val Thr Thr
67          115          120          125
69 tca gga tat tgg aaa gcc acc gga gct gat agg atg atc aga tcg gag 432
70 Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Arg Met Ile Arg Ser Glu
71          130          135          140
73 act tct cgg cct atc gga tta aag aaa acc cta gtt ttc tac tct ggt 480
74 Thr Ser Arg Pro Ile Gly Leu Lys Lys Thr Leu Val Phe Tyr Ser Gly
75 145          150          155          160
77 aaa gcc cct aaa ggc act cgt act agt tgg atc atg aac gag tat cgt 528
78 Lys Ala Pro Lys Gly Thr Arg Thr Ser Trp Ile Met Asn Glu Tyr Arg
79          165          170          175
81 ctt ccg cac cat gaa acc gag aag tac caa aag gct gaa ata tca ttg 576
82 Leu Pro His His Glu Thr Glu Lys Tyr Gln Lys Ala Glu Ile Ser Leu
83          180          185          190
85 tgc cga gtg tac aaa agg cca gga gta gaa gat cat cca tcg gta cca 624
86 Cys Arg Val Tyr Lys Arg Pro Gly Val Glu Asp His Pro Ser Val Pro
87          195          200          205
89 cgt tct ctc tcc aca aga cat cat aac cat aac tca tcg aca tca tcc 672
90 Arg Ser Leu Ser Thr Arg His His Asn His Asn Ser Ser Thr Ser Ser
91          210          215          220
93 cgt tta gcc tta aga caa caa caa cac cat tca tcc tcc tct aat cat 720
94 Arg Leu Ala Leu Arg Gln Gln Gln His His Ser Ser Ser Ser Asn His
95 225          230          235          240
97 tcc gac aac aac ctt aac aac aac aac aac atc aac aat ctc gag aag 768
98 Ser Asp Asn Asn Leu Asn Asn Asn Asn Asn Ile Asn Asn Leu Glu Lys
99          245          250          255
101 ctc tcc acc gaa tat tcc ggc gac ggc agc aca aca aca acg acc aca 816
102 Leu Ser Thr Glu Tyr Ser Gly Asp Gly Ser Thr Thr Thr Thr Thr Thr
103          260          265          270
105 aac agt aac tct gac gtt acc att gct cta gcc aat caa aac ata tat 864
106 Asn Ser Asn Ser Asp Val Thr Ile Ala Leu Ala Asn Gln Asn Ile Tyr
107          275          280          285
109 cgt cca atg cct tac gac aca agc aac aac aca ttg ata gtc tct acg 912
110 Arg Pro Met Pro Tyr Asp Thr Ser Asn Asn Thr Leu Ile Val Ser Thr
111          290          295          300
113 aga aat cat caa gac gat gat gaa act gcc att gtt gac gat ctt caa 960
114 Arg Asn His Gln Asp Asp Asp Glu Thr Ala Ile Val Asp Asp Leu Gln
115 305          310          315          320
117 aga cta gtt aac tac caa ata tca gat gga gcg aca acg cta atg cct 1008
118 Arg Leu Val Asn Tyr Gln Ile Ser Asp Gly Ala Thr Thr Leu Met Pro
119          325          330          335
121 caa act caa gcg gcg tta gct atg aac atg att cct gca gga acg att 1056
122 Gln Thr Gln Ala Ala Leu Ala Met Asn Met Ile Pro Ala Gly Thr Ile
123          340          345          350
125 cca aac aat gct ttg tgg gat atg tgg aat cca ata gta cca gat gga 1104
126 Pro Asn Asn Ala Leu Trp Asp Met Trp Asn Pro Ile Val Pro Asp Gly

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127          355          360          365
129 aac aga gat cac tat act aat att cct ttt aag taa          1140
130 Asn Arg Asp His Tyr Thr Asn Ile Pro Phe Lys
131          370          375
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 379
136 <212> TYPE: PRT
137 <213> ORGANISM: Arabidopsis thaliana
139 <400> SEQUENCE: 2
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142 Val Asn Asn Asn Glu Lys Gly Ile Glu Asp Asn Asp His Arg Gly Gly
143          20          25          30
144 Gln Glu Ser His Val Gln Asn Glu Asp Glu Ala Asp Asp His Asp His
145          35          40          45
146 Asp Met Val Met Pro Gly Phe Arg Phe His Pro Thr Glu Glu Glu Leu
147          50          55          60
148 Ile Glu Phe Tyr Leu Arg Arg Lys Val Glu Gly Lys Arg Phe Asn Val
149 65          70          75          80
150 Glu Leu Ile Thr Phe Leu Asp Leu Tyr Arg Tyr Asp Pro Trp Glu Leu
151          85          90          95
152 Pro Ala Met Ala Ala Ile Gly Glu Lys Glu Trp Tyr Phe Tyr Val Pro
153          100          105          110
154 Arg Asp Arg Lys Tyr Arg Asn Gly Asp Arg Pro Asn Arg Val Thr Thr
155          115          120          125
156 Ser Gly Tyr Trp Lys Ala Thr Gly Ala Asp Arg Met Ile Arg Ser Glu
157          130          135          140
158 Thr Ser Arg Pro Ile Gly Leu Lys Lys Thr Leu Val Phe Tyr Ser Gly
159 145          150          155          160
160 Lys Ala Pro Lys Gly Thr Arg Thr Ser Trp Ile Met Asn Glu Tyr Arg
161          165          170          175
162 Leu Pro His His Glu Thr Glu Lys Tyr Gln Lys Ala Glu Ile Ser Leu
163          180          185          190
164 Cys Arg Val Tyr Lys Arg Pro Gly Val Glu Asp His Pro Ser Val Pro
165          195          200          205
166 Arg Ser Leu Ser Thr Arg His Asn His Asn Ser Ser Thr Ser Ser
167          210          215          220
168 Arg Leu Ala Leu Arg Gln Gln Gln His His Ser Ser Ser Ser Asn His
169 225          230          235          240
170 Ser Asp Asn Asn Leu Asn Asn Asn Asn Asn Ile Asn Asn Leu Glu Lys
171          245          250          255
172 Leu Ser Thr Glu Tyr Ser Gly Asp Gly Ser Thr Thr Thr Thr Thr Thr
173          260          265          270
174 Asn Ser Asn Ser Asp Val Thr Ile Ala Leu Ala Asn Gln Asn Ile Tyr
175          275          280          285
176 Arg Pro Met Pro Tyr Asp Thr Ser Asn Asn Thr Leu Ile Val Ser Thr
177          290          295          300
178 Arg Asn His Gln Asp Asp Asp Glu Thr Ala Ile Val Asp Asp Leu Gln
179 305          310          315          320

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180 Arg Leu Val Asn Tyr Gln Ile Ser Asp Gly Ala Thr Thr Leu Met Pro
181                               325                               330                               335
182 Gln Thr Gln Ala Ala Leu Ala Met Asn Met Ile Pro Ala Gly Thr Ile
183                               340                               345                               350
184 Pro Asn Asn Ala Leu Trp Asp Met Trp Asn Pro Ile Val Pro Asp Gly
185                               355                               360                               365
186 Asn Arg Asp His Tyr Thr Asn Ile Pro Phe Lys
187                               370                               375
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191 <211> LENGTH: 2606
192 <212> TYPE: DNA
193 <213> ORGANISM: Arabidopsis thaliana
195 <220> FEATURE:
196 <221> NAME/KEY: gene
197 <222> LOCATION: (1)...(2606)
198 <223> OTHER INFORMATION: genomic DNA of LOV1 gene
200 <400> SEQUENCE: 3
201 atggcaattg tactctccac aacaagcatc attcccatga gtaaccaagt caacaataac 60
202 gaaaaaggta tagaagacaa tgatcataga ggcgggccaag agagtcatgt ccaaaatgaa 120
203 gatgaagctg atgatcatga tcatgacatg gtcatgcccg gatttagatt ccactctacc 180
204 gaagaagaac tcatagagtt ttaccttcgc cgaaaagtgt aaggcaaacg ctttaagtga 240
205 gaactcatca ctttctcga tctttatcgc tatgatcctt gggaaacttc tggtaaatat 300
206 acattcacat aaacacacat aaatcatctc aaactatttg gaaatcttaa tttctattca 360
207 tatgttaaga tctttcttct ctcttatcac tttctctctc tatttctttt tttttaacct 420
208 atatatgtac ctactcctct atgaagtatt actatgtcga tcgttaacaa ttctcaatat 480
209 ctttaaacgc ttctccctct ttagtttctt tcttaaatga acctaattaa acaacctaca 540
210 tatatatcat aagatatata aatatgtgta tgttttcata attagcttat gtatgtttaa 600
211 tcatagatat atgtatatgc agctatggcg gcgataggag agaaagagtg gtacttctat 660
212 gtgccaaagag atcggaataa tagaaatgga gatagaccga accgagtaac gacttcagga 720
213 tattggaaag ccaccggagc tgataggatg atcagatcgg agacttctcg gcctatcgga 780
214 ttaaagaaaa ccctagtttt ctactctggg aaagccccta aaggcactcg tactagtgtg 840
215 atcatgaacg agtatcgtct tccgcaccat gaaaccgaga agtaccaaaa ggtataaatt 900
216 ctactataac tctatatata tcctattcat acatacatag atataaccct agctagggtg 960
217 tgaggccttt aaaattgaaa ttaatcccta gacagtttga attttttctt ttttgactag 1020
218 ttttatttat ttattttgga attgattcga taagatcaaa aatacttgtg aatggactaa 1080
219 atgtcaggcg gcgtttgcgc ttaaattccag aaaaatgttc atgtcatatg cgtgaactct 1140
220 ttaaattgct agacatggcc catatgttat agtagaatac attaatagat agatgcatac 1200
221 acatatatat aaacacacaa gtatcacact cgacattcat ataccttaat tctgcagaga 1260
222 catagttagt ttttcttaca atttatgaca tgaatgttcc tgctcttctc cacattaatt 1320
223 catgtcttct atttaagtta cccaacattt tttgaaataa tttggcatat atgaattata 1380
224 ccaacatatt tatatgcgaa catttaaaat ctatacgaat gataacggtt tatggagtag 1440
225 accgaaaaaa tattatgtat acggaaaaatg acaatggata gataaataca ttttttgggc 1500
226 tctttcgact tatatgtcgt caccatttga aaccataaat ttataaaatt ttctatgtat 1560
227 atatatgata ttatgatgta tgcataagac agctaaaaca acagggttga cataattatc 1620
228 tatgtgtatg tattgcacat tcacttgtac taataaaact aaaattacgc aattaaatat 1680
229 ataaaaaata ataaatataa tcatcttaat tatatttgca ttgttacgtc atatgatagt 1740
230 actctaaatt tcttctaaac gtgctatctt tttttgctaa tgctaacttt acatagtttg 1800
231 tgaatcttct ttcaaaacca tatcttcgat aaatgatatt tttcatagat attgttagtc 1860
232 tatatttgat aatttgatat atgtatcaag tctctaatac atgtgctcat gtataattat 1920

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233 aggctgaaat atcattgtgc cgagtgtaca aaaggccagg agtagaagat catccatcgg 1980
234 taccacgttc tctctccaca agacatcata accataactc atcgacatca tcccgttttag 2040
235 ccttaagaca acaacaacac cattcatact cctctaataca ttccgacaac aaccttaaca 2100
236 acaacaacaa catcaacaat ctcgagaagc tctccaccga atattccggc gacggcagca 2160
237 caacaacaac gaccacaaac agtaactctg acgtttaccat tgctctagcc aatcaaaaca 2220
238 tatatcgctc aatgccttac gacacaagca acaacacatt gatagtctct acgagaaatc 2280
239 atcaagacga tgatgaaact gccattgttg acgatcttca aagactagtt aactaccaa 2340
240 tatcagatgg aggtaacatc aatcaccaat actttcaaact tgctcaacag tttcatcata 2400
241 ctcaacaaca aaatgctaac gcaaacgcac tacaattggg ggctgcggcg actacagcga 2460
242 caacgctaata gcctcaaaact caagcggcgt tagctatgaa catgattcct gcaggaacga 2520
243 ttccaaacaa tgctttgtgg gatattgtga atccaatagt accagatgga aacagagatc 2580
244 actatactaa tttcctttt aagtaa 2606
246 <210> SEQ ID NO: 4
247 <211> LENGTH: 32
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Sense primer of LOV1
254 <400> SEQUENCE: 4
255 aatagatctg gtacgcgaca tccatattga aa 32
257 <210> SEQ ID NO: 5
258 <211> LENGTH: 31
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Antisense primer of LOV1
265 <400> SEQUENCE: 5
266 aatagatctc atgggaatga tgcttgttgt g 31
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 27
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Sense primer of FLC
276 <400> SEQUENCE: 6
277 cccgttaact gaacccaaac ctgagga 27
279 <210> SEQ ID NO: 7
280 <211> LENGTH: 24
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Antisense primer of FLC
287 <400> SEQUENCE: 7
288 ccactagtcg cccttatcag cgga 24
290 <210> SEQ ID NO: 8
291 <211> LENGTH: 27
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/780,703

DATE: 10/18/2004

TIME: 10:07:08

Input Set : A:\012670-105.ST25.txt

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